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Reviewer: Anne Corrigan

Timestamp: [year=2011; month=6; day=14; hr=12; min=30; sec=34; ms=970; ]

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Application No: 09232488 Version No: 2.1

Input Set:

Output Set:

Started: 2011-06-14 12:28:30.842  
Finished: 2011-06-14 12:28:32.374  
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 532 ms  
Total Warnings: 0  
Total Errors: 0  
No. of SeqIDs Defined: 27  
Actual SeqID Count: 27

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Garner, Ian  
Dalrymple, Michael A  
Prunkard, Donna E  
Foster, Donald C

(ii) TITLE OF INVENTION: Production of Fibrinogen in Transgenic  
Animals

(iii) NUMBER OF SEQUENCES: 27

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ZymoGenetics, Inc.  
(B) STREET: 4225 Roosevelt Way, N.E.  
(C) CITY: Seattle  
(D) STATE: WA  
(E) COUNTRY: USA  
(F) ZIP: 98105

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09232488  
(B) FILING DATE: 15-JAN-1999  
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/206,176  
(B) FILING DATE: 03-MAR-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Parker, Gary E  
(B) REGISTRATION NUMBER: 31-648  
(C) REFERENCE/DOCKET NUMBER: 93-15

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 206-547-8080 ext 322  
(B) TELEFAX: 206-548-2329

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5943 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: Human Fibrinogen A-alpha chain

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: join(31..84, 1154..1279, 1739..1922, 3055..3200,  
3786..5210)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCTAGGAGC CAGCCCCACC CTTAGAAAAG ATG TTT TCC ATG AGG ATC GTC TGC	54
Met Phe Ser Met Arg Ile Val Cys	
1 5	
CTA GTT CTA AGT GTG GTG GGC ACA GCA TGG GTATGGCCCT TTTCATTTTT	104
Leu Val Leu Ser Val Val Gly Thr Ala Trp	
10 15	
TCTTCTTGCT TTCTCTCTGG TGTTTATTCC ACAAAGAGCC TGGAGGTCAG AGTCTACCTG	164
CTCTATGTCC TGACACACTC TTAGCTTTAT GACCCCAGGC CTGGGAGGAA ATTCCTGGG	224
TGGGCTTGAC ACCTCAAGAA TACAGGGTAA TATGACACCA AGAGGAAGAT CTTAGATGGA	284
TGAGAGTGTA CAACTACAAG GGAAACTTTA GCATCTGTCA TTCAGTCTTA CCACATTTTG	344
TTTTGTTTTG TTTTAAAAAG GGCAAGAATT ATTTGCCATC CTTGTACCTA TAAAGCCTTG	404
GTGCATTATA ATGCTAGTTA ATGGAATAAA ACATTTTATG GTAAGATTTG TTTTCTTTAG	464
TTATTAATTT CTGCTACTT GTCCATAATA AGCAGAACTT TTAGTGTTAG TACAGTTTGT	524
CTGAAAGGTT ATTGTTGTGT TTGTCAAGAC AGAAGAAAAA GCAAACGAAT TATCTTTGGA	584
AATATCTTTG CAGTATCAGA AGAGATTAGT TAGTAAGGCA ATACGCTTTT CCGCAGTAAT	644
GGTATTCTTT TAAATTATGA ATCCATCTCT AAAGGTTACA TAGAACTTG AAGGAGAGAG	704
GAACATTCAG TTAAGATAGT CTAGGTTTTT CTA CTGAAGC AGCAATTACA GGAGAAAGAG	764
CTCTACAGTA GTTTTCAACT TTCTGTCTGC AGTCATTAGT AAAAATGAAA AGGTAAAATT	824
TAACTGATTT TATAGATTCA AATAATTTTC CTTT TAGGAT GGATTCTTTA AAACCTCTAA	884
TATTTATCAA ATGCTTATTT AAGTGT CACA CACAGTTAAG AAATTTGTAC ACCTTGCTCTC	944
CTTTAATTCT CATAACA ACT CCATAAAATG GGTCC TAGGA TTTCCATTG AAGATAAGAA	1004
ACCTGAAGCT TGCCGAAGCC CTGTGTCTGC TCTCCTTAAT CTCTGTGAGA GTGCCATCTC	1064
TTCTTGGGGA CTTGTAGGCA TGCCACTGTC TCCTCTTCTG GCTAACATTG CTGTTGCTCT	1124

CTTTTGTGTA TGTGAATGAA TCTTTAAAG ACT GCA GAT AGT GGT GAA GGT GAC	1177
Thr Ala Asp Ser Gly Glu Gly Asp	
20 25	
TTT CTA GCT GAA GGA GGA GGC GTG CGT GGC CCA AGG GTT GTG GAA AGA	1225
Phe Leu Ala Glu Gly Gly Gly Val Arg Gly Pro Arg Val Val Glu Arg	
30 35 40	
CAT CAA TCT GCC TGC AAA GAT TCA GAC TGG CCC TTC TGC TCT GAT GAA	1273
His Gln Ser Ala Cys Lys Asp Ser Asp Trp Pro Phe Cys Ser Asp Glu	
45 50 55	
GAC TGG GTAAGCAGTC AGCGGGGGAA GCAGGAGATT CCTTCCCTCT GATGCTAGAG	1329
Asp Trp	
60	
GGGCTCACAG GCTGACCTGA TTGGTCCCAG AAACCTTTTTT AAATAGAAAA TAATTGAATA	1389
GTTACCTACA TAGCAAATAA AGAAAAGGAA CCTACTCCCA AGAGCACTGT TTATTACCT	1449
CCCCAACTCT GGATCATTAG TGGGTGAACA GACAGGATTT CAGTTGCATG CTCAGGCAAA	1509
ACCAGGCTCC TGAGTATTGT GGCCTCAATT TCCTGGCACC TATTTATGGC TAAGTGGACC	1569
CTCATTCCAG AGTTTCTCTG CGACCTCTAA CTAGTCCTCT TACCTACTTT TAAGCCAACT	1629
TATCTGGAAG AGAAAGGGTA GGAAGAAATG GGGGCTGCAT GGAAACATGC AAAATTATTC	1689
TGAATCTGAG AGATAGATCC TTAGTGTAAT TTTCTCCCTT CACTTTCAG AAC TAC	1744
Asn Tyr	
AAA TGC CCT TCT GGC TGC AGG ATG AAA GGG TTG ATT GAT GAA GTC AAT	1792
Lys Cys Pro Ser Gly Cys Arg Met Lys Gly Leu Ile Asp Glu Val Asn	
65 70 75	
CAA GAT TTT ACA AAC AGA ATA AAT AAG CTC AAA AAT TCA CTA TTT GAA	1840
Gln Asp Phe Thr Asn Arg Ile Asn Lys Leu Lys Asn Ser Leu Phe Glu	
80 85 90	
TAT CAG AAG AAC AAT AAG GAT TCT CAT TCG TTG ACC ACT AAT ATA ATG	1888
Tyr Gln Lys Asn Asn Lys Asp Ser His Ser Leu Thr Thr Asn Ile Met	
95 100 105 110	
GAA ATT TTG AGA GGC GAT TTT TCC TCA GCC AAT A GTAAGTATTA	1932
Glu Ile Leu Arg Gly Asp Phe Ser Ser Ala Asn	
115 120	
CATATTTACT TCTTTGACTT TATAACAGAA ACAACAAAAA TCCTAAATAA ATATGATATC	1992
CGCTTATATC TATGACAATT TCATCCCAAA GACTTAGTG TAGAAACACA TACCTTCATA	2052
ATATCCCTGA AAATTTTAAG AGGGAGCTTT TGTTCGTT ATTTTTCAA AGTAAAAGAT	2112
GTAACTGAG ATTGTTTAAG GTCACAAAAT AAGTCAGAAT TTTGGATTAA AACAAGAATT	2172

TAAATGTGTT CTTTTCAACA GTATATACTG AAAGTAGGAT GGGTCAGACT CTTTGAGTTG	2232
ATATTTTTGT TTCTGCTTTG TAAAGGTGAA AACTGAGAGG TCAAGGAACT TGTTCAAAGA	2292
CACAGAGCTG GGAATTCAAC TCCCAGACTC CACTGAGCTG ATTAGGTAGA TTTTAAATT	2352
TAAAATATAG GGTCAAGCTA CGTCATTCTC ACAGTCTACT CATTAGGGTT AGGAAACATT	2412
GCATTCCTC TGGGCATGGA CAGCGAGTCT AGGGAGTCCT CAGTTTCTCA AGTTTGCTT	2472
TGCCTTTTTA CACCTTCACA AACACTTGAC ATTTAAAAATC AGTGATGCCA AACTAGCTG	2532
GCAAGTGAGT GATCCTGTTG ACCCAAACA GCTTAGGAAC CATTTCAAAT CTATAGAGTT	2592
AAAAAGAAAA GCTCATCAGT AAGAAAATCC AATATGTTCA AGTCCCTGA TTAAGGATGT	2652
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TTCCAAAGAA AGTTCTTCTT CTATATTTCT TTGGGATTAC TAATTGCTAT TAGGACATCT	2772
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TTTCTTTCTT TCTTTTTTCT CTTTCTTTCT TTCTTTCTTT CTTTCTTTCT TTCTTTCTTT	2952
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ATCACTCAGC AGCTACTTCA ATAACCATAT TTTCGATTTC AG AC CGT GAT AAT	3065
	Asn Arg Asp Asn
	125
ACC TAC AAC CGA GTG TCA GAG GAT CTG AGA AGC AGA ATT GAA GTC CTG	3113
Thr Tyr Asn Arg Val Ser Glu Asp Leu Arg Ser Arg Ile Glu Val Leu	
	130 135 140
AAG CGC AAA GTC ATA GAA AAA GTA CAG CAT ATC CAG CTT CTG CAG AAA	3161
Lys Arg Lys Val Ile Glu Lys Val Gln His Ile Gln Leu Leu Gln Lys	
	145 150 155
AAT GTT AGA GCT CAG TTG GTT GAT ATG AAA CGA CTG GAG GTAAGTATGT	3210
Asn Val Arg Ala Gln Leu Val Asp Met Lys Arg Leu Glu	
	160 165 170
GGCTGTGGTC CCGAGTGTCC TTGTTTTTGA GTAGAGGGAA AAGGAAGGCG ATAGTTATGC	3270
ACTGAGTGTC TACTATATGC AGAGAAAAGT GTTATATCCA TCATCTACCT AAAAGTAGGT	3330
ATTATTTTCC TCACTCCACA GTTGAAGAAA AAAAAATTCA GAGATATTAA GTAAATTTTC	3390
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ATCACCACAC CTCTGAGCCC TCAGCCTGAG TTCACCAAGG ATCATTTAAT TAGCGTTTCC	3510
TTTGAGAGGG AATAGCACCT TACTCTTGAT CCATTCTGAG GCTAAGATGA ATTAAACAGC	3570
ATCCATTGCT TATCCTGGCT AGCCCTGCAA TACCCAACAT CTCTTCCACT GAGGGTGCTC	3630

GATAGGCAGA AAACAGAGAA TATTAAGTGG TAGGTCTCCG AGTCAAAAAA AATGAAACCA	3690
GTTTCCAGAA GGAAATTAA CTACCAGGAA CTCAATAGAC GTAGTTTATG TATTTGTATC	3750
TACATTTTCT CTTTATTTTT CTCCCCTCTC TCTAG GTG GAC ATT GAT ATT AAG	3803
Val Asp Ile Asp Ile Lys	175
ATC CGA TCT TGT CGA GGG TCA TGC AGT AGG GCT TTA GCT CGT GAA GTA	3851
Ile Arg Ser Cys Arg Gly Ser Cys Ser Arg Ala Leu Ala Arg Glu Val	
180 185 190	
GAT CTG AAG GAC TAT GAA GAT CAG CAG AAG CAA CTT GAA CAG GTC ATT	3899
Asp Leu Lys Asp Tyr Glu Asp Gln Gln Lys Gln Leu Glu Gln Val Ile	
195 200 205	
GCC AAA GAC TTA CTT CCC TCT AGA GAT AGG CAA CAC TTA CCA CTG ATA	3947
Ala Lys Asp Leu Leu Pro Ser Arg Asp Arg Gln His Leu Pro Leu Ile	
210 215 220	
AAA ATG AAA CCA GTT CCA GAC TTG GTT CCC GGA AAT TTT AAG AGC CAG	3995
Lys Met Lys Pro Val Pro Asp Leu Val Pro Gly Asn Phe Lys Ser Gln	
225 230 235 240	
CTT CAG AAG GTA CCC CCA GAG TGG AAG GCA TTA ACA GAC ATG CCG CAG	4043
Leu Gln Lys Val Pro Pro Glu Trp Lys Ala Leu Thr Asp Met Pro Gln	
245 250 255	
ATG AGA ATG GAG TTA GAG AGA CCT GGT GGA AAT GAG ATT ACT CGA GGA	4091
Met Arg Met Glu Leu Glu Arg Pro Gly Gly Asn Glu Ile Thr Arg Gly	
260 265 270	
GGC TCC ACC TCT TAT GGA ACC GGA TCA GAG ACG GAA AGC CCC AGG AAC	4139
Gly Ser Thr Ser Tyr Gly Thr Gly Ser Glu Thr Glu Ser Pro Arg Asn	
275 280 285	
CCT AGC AGT GCT GGA AGC TGG AAC TCT GGG AGC TCT GGA CCT GGA AGT	4187
Pro Ser Ser Ala Gly Ser Trp Asn Ser Gly Ser Ser Gly Pro Gly Ser	
290 295 300	
ACT GGA AAC CGA AAC CCT GGG AGC TCT GGG ACT GGA GGG ACT GCA ACC	4235
Thr Gly Asn Arg Asn Pro Gly Ser Ser Gly Thr Gly Gly Thr Ala Thr	
305 310 315 320	
TGG AAA CCT GGG AGC TCT GGA CCT GGA AGT GCT GGA AGC TGG AAC TCT	4283
Trp Lys Pro Gly Ser Ser Gly Pro Gly Ser Ala Gly Ser Trp Asn Ser	
325 330 335	
GGG AGC TCT GGA ACT GGA AGT ACT GGA AAC CAA AAC CCT GGG AGC CCT	4331
Gly Ser Ser Gly Thr Gly Ser Thr Gly Asn Gln Asn Pro Gly Ser Pro	
340 345 350	
AGA CCT GGT AGT ACC GGA ACC TGG AAT CCT GGC AGC TCT GAA CGC GGA	4379
Arg Pro Gly Ser Thr Gly Thr Trp Asn Pro Gly Ser Ser Glu Arg Gly	
355 360 365	

AGT GCT GGG CAC TGG ACC TCT GAG AGC TCT GTA TCT GGT AGT ACT GGA	4427
Ser Ala Gly His Trp Thr Ser Glu Ser Ser Val Ser Gly Ser Thr Gly	
370 375 380	
CAA TGG CAC TCT GAA TCT GGA AGT TTT AGG CCA GAT AGC CCA GGC TCT	4475
Gln Trp His Ser Glu Ser Gly Ser Phe Arg Pro Asp Ser Pro Gly Ser	
385 390 395 400	
GGG AAC GCG AGG CCT AAC AAC CCA GAC TGG GGC ACA TTT GAA GAG GTG	4523
Gly Asn Ala Arg Pro Asn Asn Pro Asp Trp Gly Thr Phe Glu Glu Val	
405 410 415	
TCA GGA AAT GTA AGT CCA GGG ACA AGG AGA GAG TAC CAC ACA GAA AAA	4571
Ser Gly Asn Val Ser Pro Gly Thr Arg Arg Glu Tyr His Thr Glu Lys	
420 425 430	
CTG GTC ACT TCT AAA GGA GAT AAA GAG CTC AGG ACT GGT AAA GAG AAG	4619
Leu Val Thr Ser Lys Gly Asp Lys Glu Leu Arg Thr Gly Lys Glu Lys	
435 440 445	
GTC ACC TCT GGT AGC ACA ACC ACC ACG CGT CGT TCA TGC TCT AAA ACC	4667
Val Thr Ser Gly Ser Thr Thr Thr Thr Arg Arg Ser Cys Ser Lys Thr	
450 455 460	
GTT ACT AAG ACT GTT ATT GGT CCT GAT GGT CAC AAA GAA GTT ACC AAA	4715
Val Thr Lys Thr Val Ile Gly Pro Asp Gly His Lys Glu Val Thr Lys	
465 470 475 480	
GAA GTG GTG ACC TCC GAA GAT GGT TCT GAC TGT CCC GAG GCA ATG GAT	4763
Glu Val Val Thr Ser Glu Asp Gly Ser Asp Cys Pro Glu Ala Met Asp	
485 490 495	
TTA GGC ACA TTG TCT GGC ATA GGT ACT CTG GAT GGG TTC CGC CAT AGG	4811
Leu Gly Thr Leu Ser Gly Ile Gly Thr Leu Asp Gly Phe Arg His Arg	
500 505 510	
CAC CCT GAT GAA GCT GCC TTC TTC GAC ACT GCC TCA ACT GGA AAA ACA	4859
His Pro Asp Glu Ala Ala Phe Phe Asp Thr Ala Ser Thr Gly Lys Thr	
515 520 525	
TTC CCA GGT TTC TTC TCA CCT ATG TTA GGA GAG TTT GTC AGT GAG ACT	4907
Phe Pro Gly Phe Phe Ser Pro Met Leu Gly Glu Phe Val Ser Glu Thr	
530 535 540	
GAG TCT AGG GGC TCA GAA TCT GGC ATC TTC ACA AAT ACA AAG GAA TCC	4955
Glu Ser Arg Gly Ser Glu Ser Gly Ile Phe Thr Asn Thr Lys Glu Ser	
545 550 555 560	
AGT TCT CAT CAC CCT GGG ATA GCT GAA TTC CCT TCC CGT GGT AAA TCT	5003
Ser Ser His His Pro Gly Ile Ala Glu Phe Pro Ser Arg Gly Lys Ser	
565 570 575	
TCA AGT TAC AGC AAA CAA TTT ACT AGT AGC ACG AGT TAC AAC AGA GGA	5051
Ser Ser Tyr Ser Lys Gln Phe Thr Ser Ser Thr Ser Tyr Asn Arg Gly	
580 585 590	
GAC TCC ACA TTT GAA AGC AAG AGC TAT AAA ATG GCA GAT GAG GCC GGA	5099



Asp Ser Thr Phe Glu Ser Lys Ser Tyr Lys Met Ala Asp Glu Ala Gly	
595 600 605	
AGT GAA GCC GAT CAT GAA GGA ACA CAT AGC ACC AAG AGA GGC CAT GCT	5147
Ser Glu Ala Asp His Glu Gly Thr His Ser Thr Lys Arg Gly His Ala	
610 615 620	
AAA TCT CGC CCT GTC AGA GGT ATC CAC ACT TCT CCT TTG GGG AAG CCT	5195
Lys Ser Arg Pro Val Arg Gly Ile His Thr Ser Pro Leu Gly Lys Pro	
625 630 635 640	
TCC CTG TCC CCC TAGACTAAGT TAAATATTTT TGCACAGTGT TCCCATGGCC	5247
Ser Leu Ser Pro	
CCTTGCATTT CCTTCTTAAC TCTCTGTTAC ACGTCATTGA AACTACACTT TTTTGGTCTG	5307
TTTTTGTGCT AGACTGTAAAG TTCCTTGGGG GCAGGGCCTT TGTCTGTCTC ATCTCTGTAT	5367
TCCCAAATGC CTAACAGTAC AGAGCCATGA CTCAATAAAT ACATGTTAAA TGGATGAATG	5427
AATTCCTCTG AAACTCTATT TGAGCTTATT TAGTCAAATT CTTTCACTAT TCAAAGTGTG	5487
TGCTATTAGA ATTGTCACCC AACTGATTAA TCACATTTTT AGTATGTGTC TCAGTTGACA	5547
TTTAGGTCAG GCTAAATACA AGTTGTGTTA GTATTAAGTG AGCTTAGCTA CCTGTACTGG	5607
TTACTTGCTA TTAGTTTGTG CAAGTAAAAT TCCAAATACA TTTGAGGAAA ATCCCCTTTG	5667
CAATTTGTAG GTATAAATAA CCGCTTATTT GCATAAGTTC TATCCCACTG TAAGTGCATC	5727
CTTTCCTTAT GGAGGGAAGG AAAGGAGGAA GAAAGAAAGG AAGGGAAAGA AACAGTATTT	5787
GCCTTATTTA ATCTGAGCCG TGCCTATCTT TGTAAGTTA AATGAGAATA ACTTCTTCCA	5847
ACCAGCTTAA TTTTTTTTTT AGACTGTGAT GATGTCCTCC AAACACATCC TTCAGGTACC	5907
CAAAGTGGCA TTTTCAATAT CAAGCTATCC GGATCC	5943

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Phe Ser Met Arg Ile Val Cys Leu Val Leu Ser Val Val Gly Thr	
1 5 10 15	
Ala Trp Thr Ala Asp Ser Gly Glu Gly Asp Phe Leu Ala Glu Gly Gly	
20 25 30	

Gly	Val	Arg	Gly	Pro	Arg	Val	Val	Glu	Arg	His	Gln	Ser	Ala	Cys	Lys	35	40	45
Asp	Ser	Asp	Trp	Pro	Phe	Cys	Ser	Asp	Glu	Asp	Trp	Asn	Tyr	Lys	Cys	50	55	60
Pro	Ser	Gly	Cys	Arg	Met	Lys	Gly	Leu	Ile	Asp	Glu	Val	Asn	Gln	Asp	65	70	75
Phe	Thr	Asn	Arg	Ile	Asn	Lys	Leu	Lys	Asn	Ser	Leu	Phe	Glu	Tyr	Gln	85	90	95
Lys	Asn	Asn	Lys	Asp	Ser	His	Ser	Leu	Thr	Thr	Asn	Ile	Met	Glu	Ile	100	105	110
Leu	Arg	Gly	Asp	Phe	Ser	Ser	Ala	Asn	Asn	Arg	Asp	Asn	Thr	Tyr	Asn	115	120	125
Arg	Val	Ser	Glu	Asp	Leu	Arg	Ser	Arg	Ile	Glu	Val	Leu	Lys	Arg	Lys	130	135	140
Val	Ile	Glu	Lys	Val	Gln	His	Ile	Gln	Leu	Leu	Gln	Lys	Asn	Val	Arg	145	150	155
Ala	Gln	Leu	Val	Asp	Met	Lys	Arg	Leu	Glu	Val	Asp	Ile	Asp	Ile	Lys	165	170	175
Ile	Arg	Ser	Cys	Arg	Gly	Ser	Cys	Ser	Arg	Ala	Leu	Ala	Arg	Glu	Val	180	185	190
Asp	Leu	Lys	Asp	Tyr	Glu	Asp	Gln	Gln	Lys	Gln	Leu	Glu	Gln	Val	Ile	195	200	205
Ala	Lys	Asp	Leu	Leu	Pro	Ser	Arg	Asp	Arg	Gln	His	Leu	Pro	Leu	Ile	210	215	220
Lys	Met	Lys	Pro	Val	Pro	Asp	Leu	Val	Pro	Gly	Asn	Phe	Lys	Ser	Gln	225	230	235
Leu	Gln	Lys	Val	Pro	Pro	Glu	Trp	Lys	Ala	Leu	Thr	Asp	Met	Pro	Gln	245	250	255
Met	Arg	Met	Glu	Leu	Glu	Arg	Pro	Gly	Gl									